

1 ATGCTGTTCCGCCCGGGGGCGGTACGGGCAGGGCTGGGGCGGCCGGAGGCT 60
 1 M L F R A R G P V R G R G W G R P A E A 20

 61 CCCCCGCCGGCGCTGCCGCCCTGGAGCCCCGCTGGATTTGCTGCTGGCGCTGCC 120
 21 P R R G R S P P W S P A W I C C W A L A 40

 121 GGCTGCCAGGCAGCTGGCTGGGACCTGCCCTCCTCCAGCCGCCGCTCCTCCT 180
 41 G C Q A A W A G D L P S S S S R P L P P 60

 181 TGCCACGGAGAAAGATTATCACTTGAATATAAGGAATGTGATAGCAGTGGCTCCAGGTGG 240
 61 C Q E K D Y H F E Y T E C D S S S G S R W 80

 241 AGAGTTGCCATTCAAATTCTGCAGTGGACTGCTCTGGCTGCCTGACCCAGTGAGAGGC 300
 81 R V A I P N S A V D C S G L P D P V R G 100

 301 AAAGAATGCACTTCTCTGTGCTTCTGGAGAGTATCTAGAAATGAAGAACCAAGGTATGC 360
 101 K E C T F S C A S G E Y L E M K N Q V C 120

 361 AGTAAGTGTGGTAAGGCACCTATTCTGGCAGTGGCATCAAATTGATGAATGGGAT 420
 121 S K C G E G T Y S L G S G I K F D E W D 140

 421 GAATTGCCGGCAGGATTTCTAACATCGAACATTGACACTGTGGTGGCCCTCT 480
 141 E L P A G F S N I A T F M D T V V G P S 160

 481 GACAGCAGGCCAGACGGCTGTAACAACCTTCTGGATCCCTCGTGGAAACTACATAGAA 540
 161 D S R P D G C N N S S W I P R G N Y I E 180

 541 TCTAACCGTGTACTGCACGGTGTGGATCTATGCTGTGCACCTTAAGAAGTCAGGC 600
 181 S N R D D C T V S L I Y A V H L K K S G 200

 601 TATGTCTTCTTGAGTACCAAGTATGTCGACAACAACATCTCTTGAGTTCTTATTCAA 660
 201 Y V F F E Y Q Y V D N N I F F E F F I Q 220

FIG. 1A

661 AATGATCAGTGCCAGGAGATGGACACCACACTGACAAGTGGTAAAACCTACAGACAAT 720
 221 N D Q C Q E M D T T D K W V K L T D N 240

 721 GGAGAATGGGGCTCTCATTCTGTAATGCTGAAATCAGGCACAAACATACTCTACTGGAGA 780
 241 G E W G S H S V M L K S G T N I L Y W R 260

 781 ACTACAGGCATCCTTAIGGGTTCTAAGGCCGTCAAGCCTGTGCTGGTAAAAAATATCACA 840
 261 T T G I L M G S K A V K P V L V K N I T 280

 841 ATTGAAGGGTGGCGTACACATCAGAATGTTTCTGCAAGCCAGGCACATTAGAAC 900
 281 I E G V A Y T S E C F P C K P G T F S N 300

 901 AAACCAGGTCATTCAACTGCCAGGTGTCCCAGAAACACCTATTCTGAGAAAGGAGCC 960
 301 K P G S F N C Q V C P R N T Y S E K G A 320

 961 AAAGAATGTATAAGGTGTAAAGACGACTCTCAATTTCAGGATCCAGTGAGTGTACAGAG 1020
 321 K E C I R C K D D S Q F S G S S E C T E 340

 1021 CGCCCTCCCTGTACCACAAAAGACTATTCAGATCCATACTCCATGTGATGAAGAAGGA 1080
 341 R P P C T T K D Y F Q I H T P C D E E G 360

 1081 AAGACACAGATAATGTACAAGTGGATAGAGCCCCAAATCTGCCGGAGGATCTCACAGAT 1140
 361 K T Q I M Y K W I E P K I C R E D L T D 380

 1141 GCTATTAGATTGCCCTCTGGAGAGAAGAAGGATTGTCCGCCCTGCAACCCTGGATT 1200
 381 A I R L P P S G E K K D C P P C N P G F 400

 1201 TATAACAATGGATCATCTTCTGCCATCCCTGTCCCTGGAACATTTAGATGGAACC 1260
 401 Y N N G S S S C H P C P P G T F S D G T 420

 1261 AAAGAATGTAGACCATGTCCAGCAGGAACGGAGCCTGCACTGGCTTGAAATATAATGG 1320
 421 K E C R P C P A G T E P A L G F E Y K W 440

FIG. 1B

1321 TGGAATGTCCTCCTGGCAACATGAAAATCCTGCTCAATGTTGGATTCAAAGTGC 1380
 441 W N V L P G N M K T S C F N V G N S K C 460

1381 GATGGAATGAATGGTGGGAGGTGGCTGGAGATCATATCCAGAGTGGGCTGGAGGTTCT 1440
 461 D G M N G W E V A G D H I Q S G A G G S 480

1441 GACAATGATTACCTGATCTTAAACTGCATATCCCAGGATTAAACCACCAACATCTATG 1500
 481 D N D Y L I L N L H I P G F K P P T S M 500

1501 ACTGGAGCCACGGTTCTGAACTAGGAAGAATAACATTGTCTTGAGACCCCTGTTCA 1560
 501 T G A T G S E L G R I T F V F E T L C S 520

1561 GCTGACTGTGTTGTACTTCATGGTGGATATTAATAGAAAAAGTACAAATGTGGTAGAA 1620
 521 A D C V L Y F M V D I N R K S T N V V E 540

1621 TCGTGGGTGAAACCAAGAAAACAAGCTTACACCCATATCATCTTCAAGAACATGCAACT 1680
 541 S W G G T K E K Q A Y T H I I F K N A T 560

1681 TTTACATTTACATGGCATTCCAGAGAACTAATCAGGGTCAAGATAATAGACGGTCATC 1740
 561 F T F T W A F Q R T N Q G Q D N R R F I 580

1741 AATGACATGGTGAAGATTATTCTATCACAGCCACTAATGCAGTTGATGGGTGGCGTCC 1800
 581 N D M V K I Y S I T A T N A V D G V A S 600

1801 TCATGCCGTGCCTGTGCCCTCGGTCTGAACAGTCGGTTCATCGTGTCCCCTGCCCT 1860
 601 S C R A C A L G S E Q S G S S C V P C P 620

1861 CCAGGCCACTACATTGAGAAAGAAACCAACCAAGTGCAAGGAATGTCCACCTGACACCTAC 1920
 621 P G H Y I E K E T N Q C K E C P P D T Y 640

1921 CTGTCCATACATCAGGTCTATGGCAAAGAGGTTGTATTCCATGCCGGGCTGGAGTAAA 1980
 641 L S I H Q V Y G K E A C I P C G P G S K 660

FIG. 1C

1981	AACAATCAGGACCATTGGTTGCTATAGTGACTGCTTTCTACCATGAAAAGAAAAT	2040
661	N N Q D H S V C Y S D C F F Y H E K E N	680
2041	CAGATTTGCACTATGACTTAGAACCTCAGCAGTGTGGGCTCATTAATGAATGGCCCC	2100
681	Q I L H Y D F S N L S S V G S L M N G P	700
2101	AGCTTCACCTCAAAGGAACAAACTCCATTCTCAATATCAGTTATGTGGCAT	2160
701	S F T S K G T K Y F H F F N I S L C G H	720
2161	GAGGGAAAGAAGATGGCTCTGTACCAACAATAACAGACTTACAGTAAAGAAATA	2220
721	E G K K M A L C T N N I T D F T V K E I	740
2221	GTGGCAGGGTCAGATGATTACACAAATTGGTAGGGCATTGTATGCCAGTCAACAATT	2280
741	V A G S D D Y T N L V G A F V C Q S T I	760
2281	ATTCTCTGAAAGTAAGGTTCCGAGCAGCCTATCATCACAAATCCATCATTCTGGCA	2340
761	I P S E S K G F R A A L S S Q S I I L A	780
2341	GATACATTCAAGGAGTCACAGTTGAAACCACATTGAAAAATTAAATATAAAAGAAGAT	2400
781	D T F I G V T V E T T L K N I N I K E D	800
2401	ATGTTCCAGTTCCAACAAGCAAATACCAAGATGTGCATTCTTTATAAGTCTTCTACA	2460
801	M F P V P T S Q I P D V H F F Y K S S T	820
2461	GCAACAACATCTGTATTAAATGGCCGATCAACTGCTGTGAAATGAGGTGTAAATCCTACT	2520
821	A T T S C I N G R S T A V K M R C N P T	840
2521	AAATCTGGAGCAGGAGTGATTCACTCCCCAGCAAGTGCCCAGCAGGTACCTGTGATGGG	2580
841	K S G A G V I S V P S K C P A G T C D G	860
2581	TGTACGTTCTATTCTGTGGAGAGTGCTGAAGCTGCCCTCTGTGTACGGAGCATGAC	2640
861	C T F Y F L W E S A E A C P L C T E H D	880

FIG. 1D

2641 TTCCATGAGATTGAGGGAGCCTGCAAGAGAGGATTCAGGAACCTGTATGTGTGGAAT 2700
 881 F H E I E G A C K R G F Q E T L Y V W N 900
 2701 GAACCTAAATGGTGCATTAAAGGAATTCTTGCCTGAGAAAAGTTGGAACCTGTGAA 2760
 901 E P K W C I K G I S L P E K K L A T C E 920
 2761 ACGGTTGACTTTGGCTGAAGGTGGAGCCGGTGTGGAGCTTTACTGCCGTTTGCTG 2820
 921 T V D F W L K V G A G V G A F T A V L L 940
 2821 GTGGCTCTGACCTGCTACTCTGGAAAAAGAATCAAAGAAAAGAAGACCATTGAAAT 2880
 941 V A L T C Y F W K K N Q K K K K T I L N 960
 2881 CTGTTCAACTGAAAACCTCAAGATCCCCAAATATATGAAGAGACAGTGCTGTAGCCTG 2940
 961 L F N * 964
 2941 GACTAATGAACAAAGAAACCTGCTCTAGTTTACAGGACCATATTTAGGGCTGTCCCTC 3000
 3001 ATACCTGTCACATTGGTATCTCACAGAGGAGGCCATGCCGCTGAAAAGGAAGGAGAT 3060
 3061 TGAAACATTGATTGCCTTATCACATGGTCAAGTACCTGCCAAATAAGGAAAGCAAAT 3120
 3121 GATTGGGTCTCACTGAAGATGAAGCTCAACTCAGGAAGAGATTATCTGTATACAC 3180
 3181 ATAATGAAAACCAAGTTAAGCCCACCAATGCACTGCTGATGCATGCCATATAATTAAAT 3240
 3241 GGGTAACTTTATTCTTATGATGTCTACATAACAAGTGTGATTGGAAGGCACATGTGA 3300
 3301 GCATATGCATTATGATCCAATTATGTTTTCTTGTATATTGGGGAAAATTAAA 3360
 3361 ATTTTTTAAGGTAAAAAAAAAAAAAAA 3390

FIG. 1E

FIG. 2A

	10	20	30	
1	M L F R A R G P V R G R G W G R P A E A P R R G R S P P W S			TR16.aa
1	M - - - - - D I K N L - L T V - - -			EMB CAB41042.1 TNFR
1	M - - - - - C V G A R R L G R G P - - -			emb CAA53576.1 OX40
	40	50	60	
31	P A W I C C W A L A G C Q A A W A G D L E S S S S R E L P P			TR16.aa
10	- - - - - C T I F Y I T T L A T A D - - -			EMB CAB41042.1 TNFR
13	- - - - - C A A L L L L G L G L S T - - -			emb CAA53576.1 OX40
	70	80	90	
61	C O E K D Y H F E Y T E C D S S G S R W R V A I P N S A V D			TR16.aa
23	- - - - - I P T S S L P			EMB CAB41042.1 TNFR
26	- - - - - V - - T G L H			emb CAA53576.1 OX40
	100	110	120	
91	C S G L P D P E V R G K E C T F S C A S G E Y L E M K N Q V C			TR16.aa
30	- - - H A P V N G - - - A C D E G E Y L D K R H N Q C			EMB CAB41042.1 TNFR
31	- - - - - C V G D T Y - - P S N D R C			emb CAA53576.1 OX40
	130	140	150	
121	S K C G E G T Y S L G S G I K F D E W D E L P A G F S N I A			TR16.aa
51	- - - - -			EMB CAB41042.1 TNFR
43	- - - - -			emb CAA53576.1 OX40
	160	170	180	
151	T F M D T V V G P S D S R P D G C N N S S W I P R G N Y I E			TR16.aa
51	- - - - -			EMB CAB41042.1 TNFR
43	- - - - -			emb CAA53576.1 OX40
	190	200	210	
181	S N R D D C T V S L I Y A V H L K K S G Y V F F E Y Q Y V D			TR16.aa
51	- - - - -			EMB CAB41042.1 TNFR
43	- - - - -			emb CAA53576.1 OX40
	220	230	240	
211	N N I F F E F F I Q N D Q C O E M D T T T D K W V K L T D N			TR16.aa
51	- - - - -			EMB CAB41042.1 TNFR
43	- - - - -			emb CAA53576.1 OX40
	250	260	270	
241	G E W G S H S V M L K S G T N I L Y W R T T G I L M G S K A			TR16.aa
51	- - - - -			EMB CAB41042.1 TNFR
43	- - - - -			emb CAA53576.1 OX40
	280	290	300	
271	V K P V L V K N I T T E G V A Y T S E C F B C K P G T F S N			TR16.aa
51	- - - - -			EMB CAB41042.1 TNFR
43	- - - - -			emb CAA53576.1 OX40
	310	320	330	
301	K P G S F N C O V C P R N T Y S E K G A K E C I R C K D D S			TR16.aa
62	- - - - - V R C N - - -			EMB CAB41042.1 TNFR
54	- - - - - S R C S - - -			emb CAA53576.1 OX40

FIG. 2B

	340	350	360	
331	Q F S G S S E C T E R F P I C T K D Y - F Q I H T P C D E E G			TR16.aa
66	- - - - -	- - - - -	- - - - -	EMB CAB41042.1 TNFR
58	- - - - -	- - - - -	- - - - -	emb CAA53576.1 OX40
	370	380	390	
361	K T Q I M Y K W I E P K I C R E D L T D A I R L P P S G E K			TR16.aa
66	- - - - -	- - - - -	- G N D N	EMB CAB41042.1 TNFR
58	- - - - -	- - - - -	- R S Q N	emb CAA53576.1 OX40
	400	410	420	
391	K D C P P C N R G F Y N N G S S S C H P C P P G T F S D G T			TR16.aa
70	T K C E R C P P H T Y T A - I P N Y S N G C - - - - -	-	-	EMB CAB41042.1 TNFR
62	T V C R P C G P G F Y N D V V S - S K P C - - - - -	-	-	emb CAA53576.1 OX40
	430	440	450	
421	K E C R P C P A G T E P A L G F E Y K W W N V L P G N M K T			TR16.aa
91	H Q C R K C - - P T G S - - - - -	-	- F D K V	EMB CAB41042.1 TNFR
82	K P C T W C N L R S G S - - - - -	-	- E R K Q	emb CAA53576.1 OX40
	460	470	480	
451	S C F N V G N S K C D G M N G W E V A G D H I Q S G A G G S			TR16.aa
105	K C T G T Q N S K C S C L P G W Y C A T D S S Q T - - - - -	-	- E M B CAB41042.1 TNFR	
98	L C T A T Q D T V C R C R A G - - - T Q P L D S - - - - -	-	- emb CAA53576.1 OX40	
	490	500	510	
481	D N D Y L I L N L H I P G F K P P T S M T G A T G S E L G R			TR16.aa
130	- - - - - E D - - - - -	-	-	EMB CAB41042.1 TNFR
119	- - - - - Y K P - - - - -	-	-	emb CAA53576.1 OX40
	520	530	540	
511	I T F V F E T L C S A D C V L Y F M V D I N R K S T N V V E			TR16.aa
132	- - - - - C R D C I - - - - -	-	-	EMB CAB41042.1 TNFR
122	- - - - - G V D C A - - - - -	-	-	emb CAA53576.1 OX40
	550	560	570	
541	S W G G T K E K Q A Y T H I I F K N A T F T F T W A F Q R T			TR16.aa
137	- - - - -	-	-	EMB CAB41042.1 TNFR
127	- - - - -	-	-	emb CAA53576.1 OX40
	580	590	600	
571	N O G O D N R R F E I N D M V K I Y S I T A T N A V D G V A S			TR16.aa
137	- - - - - P K R R - - - - -	-	-	EMB CAB41042.1 TNFR
127	- - - - - P - - - - -	-	-	emb CAA53576.1 OX40
	610	620	630	
601	S C R A C A L G S E O S G S S C V P C P P G H Y I E K E T N			TR16.aa
141	- - - - - C P C G Y F - - - - -	-	-	EMB CAB41042.1 TNFR
128	- - - - - C P P G H F - - - - -	-	-	emb CAA53576.1 OX40

FIG. 2C

631 Q C K E C P P D T Y L S E H O V Y G K E A C I P C G B G S K TR16.aa
 147 - - - - - G G I E M B | CAB41042.1 TNFR
 134 - - - - - S P G emb | CAA53576.1 OX40

660

640 650 660

661 N N Q D H S V C Y S D C E F Y H E K E N Q I L H Y D F S N L TR16.aa
 150 D E Q G N P I C E M B | CAB41042.1 TNFR
 137 D N O A - - - C emb | CAA53576.1 OX40

670 680 690

691 S S V G S L M N G B S F T S K G T K Y F H F F N I S L C G H TR16.aa
 158 - - - - - K S C C V E M B | CAB41042.1 TNFR
 142 - - - - - K P W T N C T L emb | CAA53576.1 OX40

700 710 720

721 E G K K M A L C T N N I T D F T V K E I V A G S D D Y T N L TR16.aa
 163 G E - - - - - Y E M B | CAB41042.1 TNFR
 150 A G K H - - - - - T L Q P A S N S S D A I emb | CAA53576.1 OX40

730 740 750

751 V G A F V C O S T I P S E S K G F R A A L S S O S I I L A TR16.aa
 166 - - - - - C D E M B | CAB41042.1 TNFR
 166 - - - - - C E D R D P E A T Q P Q E T Q G P P A R P I T V Q emb | CAA53576.1 OX40

760 770 780

781 D T F I G V T V E T T L K N I N I K E D M F P V P T S Q I P TR16.aa
 168 - - - - - E A W P - R T S Q G P E M B | CAB41042.1 TNFR
 191 P T - - - - - emb | CAA53576.1 OX40

790 800 810

811 D V H E F Y K S S T A T T S C I N G R S T A V K M R C N P T TR16.aa
 168 - - - - - S T R P V E V P G G R A V A A I L E M B | CAB41042.1 TNFR
 203 - - - - - emb | CAA53576.1 OX40

820 830 840

841 K S G A G V I S V P S K C P A G T C D G C T F Y F L W E S A TR16.aa
 168 - - - - - L G L L E M B | CAB41042.1 TNFR
 220 - - - - - G L G L V - - - - - emb | CAA53576.1 OX40

850 860 870

871 E A C P L C T E H D F H E I E G A C K T G F O E T L Y V W N TR16.aa
 168 - - - - - Y L E M B | CAB41042.1 TNFR
 229 - - - - - A I L L A L Y L L R emb | CAA53576.1 OX40

880 890 900

901 E P K W C I K G I S L P E K K L A T C E T V D F W L K V G A TR16.aa
 170 - - - - - R N Y R L D P - - - - - P E M B | CAB41042.1 TNFR
 242 - - - - - R D Q R L E P D A H K P - - - - - emb | CAA53576.1 OX40

910 920 930

9/20

FIG. 2D

	940	.	950	.	960	
931	G V G A E T A V L L V A D T C Y E W K R N Q K K K K T I L N					TR16.aa
177	- - - F - - - - - - - - - - - - - - - P P C K L S					EMB CAB41042.1 TNFR
255	G G G S E R T P I - - - - - Q E E Q A D A H S T I L A					emb CAA53576.1 OX40

961 L F N
184 K C - N
276 K I

TR16.aa
EMB | CAB41042.1 TNFR
emb | CAA53576.1 OX40

TR16.aa

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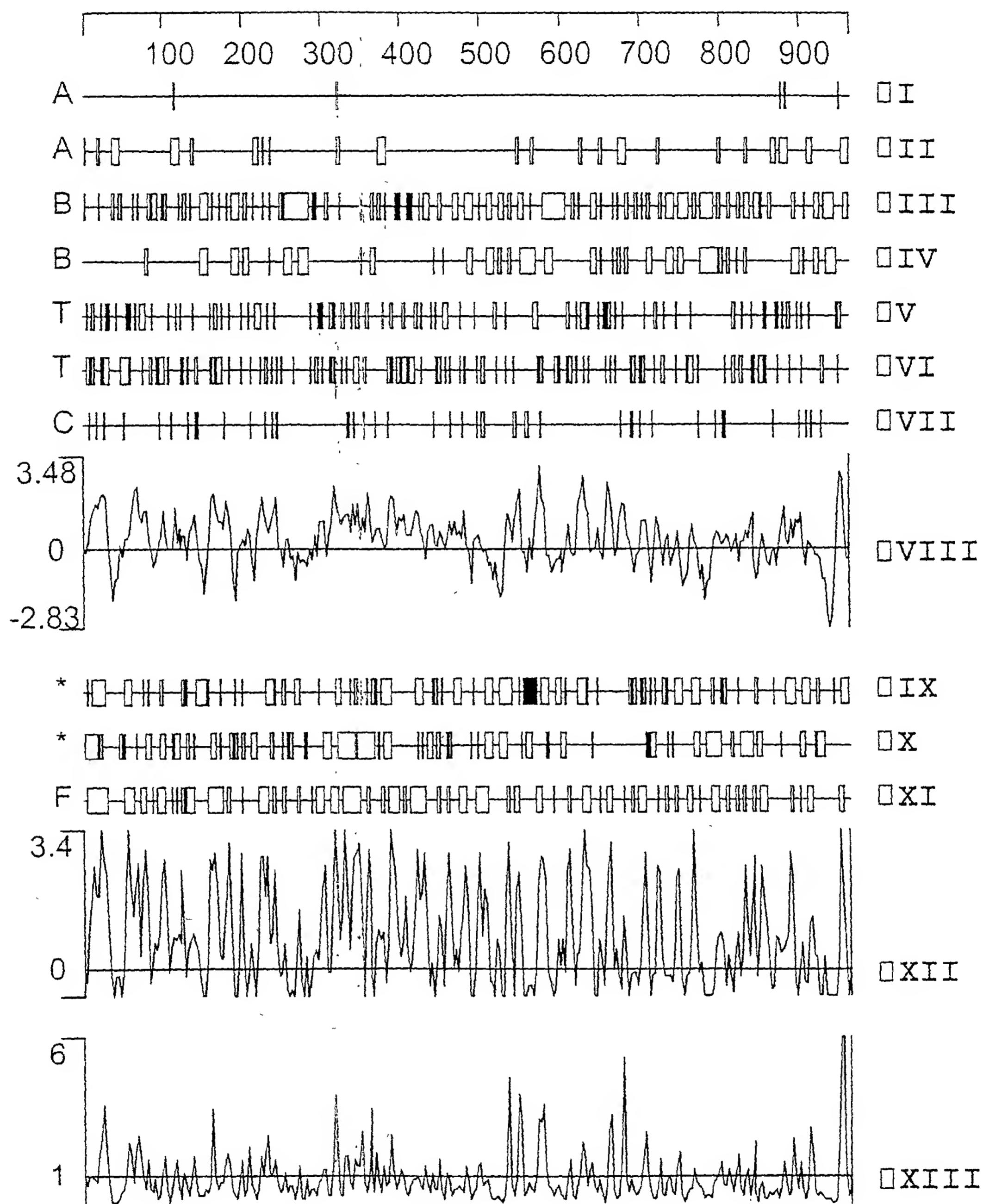


FIG. 3

1	ATGCTGTTCCGGCGCCGGGGGGCGGTACGGGGCAGGGCTGGGGCGCCGGAGGCT	60
1	M L F R A R G P V R G R G W G R P A E A	20
61	CCCCGCCGGGGCGCTGCCGCCCTGGAGCCCCGCCTGGATTGCTGCTGGCGCTGCC	120
21	P R R G R S P P W S P A W I C C C W A L A	40
121	GGCTGCCAGGCGGCCCTGGCTGGGACCTGCCCTCCCTCCAGCCGCCGCTCCCT	180
41	G C Q A A W A G D L P S S S S R P L P P	60
181	TGCCAGGAGAAAGATTATCACTTGAATATACTGGATGTGATAGCAGTGGCTCCAGGTGG	240
61	C Q E K D Y H T E Y T E C D S S S G S R W	80
241	AGAGTTGCCATTCAAATTCTGCAGTGGACTGCTCTGGCTGCCTGACCCAGTGAGAGGC	300
81	R V A I P N S A V D C S G L P D P V R G	100
301	AAAGAATGCACTTCTCCTGTGCTCTGGAGAGTATCTAGAAATGAAGAACAGGTATGC	360
101	K E C T F S C A S G E Y L E M K N Q V C	120
361	AGTAAGTGTGGTGAAGGCACCTATTCTGGCAGTGGCATCAAATTGATGAATGGAT	420
121	S K C G E G T Y S L G S G I K F D E W D	140
421	GAATTGCCGGCAGGATTTCTAACATCGAACATTGACACTGTGGTGGCCCTTCT	480
141	E L P A G F S N I A T F M D T V V G P S	160
481	GACAGCAGGCCAGACGGCTGTAAACAACACTCTTGGATCCCTCGTGGAAACTACATAGAA	540
161	D S R P D G C N N S S W I P R G N Y I E	180
541	TCTAATCGTGTGACTGCACGGTGTCTTGATCTATGCTGTGCACCTTAAGAAGTCAGGC	600
181	S N R D D C T V S L I Y A V H L K K S G	200
601	TATGTCTTCTTGAGTACCAAGTATGTCACAAACATCTTCTTGAGTTCTTATTCAA	660
201	Y V F F E Y Q Y V D N N I F F E F F I Q	220
661	AATGATCAGTGCCAGGAGATGGACACCACCTGACAAGTGGTAAAACCTACAGACAAT	720
221	N D Q C Q E M D T T D K W V K L T D N	240

FIG. 4A

721 GGAGAATGGGCTCTCATTCTGTAAATGCTGAAATCAGGCACAAACATACTCTACTGGAGA 780
 241 G E W G S H S V M L K S G T N I L Y W R 260

781 ACTACAGGCATCCTTATGGGTTCTAAGGCGGTCAAGCCTGTGCTGGTAAAAAATATCACA 840
 261 T T G I L M G S K A V K P V L V K N I T 280

841 ATTGAAGGGTGGCGTACACATCAGAATGTTTCTTGCAAGCCAGGCACATTAGAAC 900
 281 I E G V A Y T S E C F P C K P G T F S N 300

901 AAACCAGGTTCACTGCCAGGTGTCCCAGAAACACCTATTCTGAGAAAGGAGCC 960
 301 K P G S F N C Q V C P R N T Y S E K G A 320

961 AAAGAATGTATAAGGTGAAAGACGACTCTCAATTTCAGGATCCAGTGAGTGTACAGAG 1020
 321 K E C I R C K D D S Q F S G S S E C T E 340

1021 CGCCCTCCCTGTACCACAAAAGACTATTCCAGATCCATACTCCATGTGATGAAGAAGGA 1080
 341 R P P C T T K D Y F Q I H T P C D E E G 360

1081 AAGACACAGATAATGTACAAGTGGATAGAGCCCCAAATCTGCCGGAGGATCTCACAGAT 1140
 361 K T Q I M Y K W I E P K I C R E D L T D 380

1141 GCTATTAGATTGCCCTCTGGAGAGAAGAAGGATTGTCCGCCCTGCAACCCTGGATT 1200
 381 A I R L P P S G E K K D C P P C N P G F 400

1201 TATAACAATGGATCATCTTCTGCCATCCCTGTCTCTGGAACATTTAGATGGAACC 1260
 401 Y N N G S S S C H P C P P G T F S D G T 420

1261 AAAGAATGTAGACCATGTCCAGCAGGAACGGAGCCTGCACTTGGCTTGAATATAATGG 1320
 421 K E C R P C P A G T E P A L G F E Y K W 440

1321 TGGAATGTCTTCTGGCAACATGAAAATTCCTGCTCAATGTTGGAAATCAAAGTGC 1380
 441 W N V L P G N M K T S C F N V G N S K C 460

1381 GATGGAATGAATGGTGGGAGGTGGCTGGAGATCATATCCAGAGTGGGGCTGGAGGTTCT 1440
 461 D G M N G W E V A G D H I Q S G A G G S 480

FIG. 4B

1441	GACAATGATTACCTGATCTTAAACTGCATATCCCAGGATTAAACCACCAACATCTATG	1500
481	D N D Y L I L N L H I P G F K P P T S M	500
1501	ACTGGAGCCACGGTTCTGAACTAGGAAGAATAACATTGTCTTGAGACCCCTCTGTCA	1560
501	T G A T G S E L G R I T F V F E T L C S	520
1561	GCTGACTGTGTTTGTACTTCATGGTGGATATTAATAGAAAAAGTACAAATGTGGTAGAA	1620
521	A D C V L Y F M V D I N R K S T N V V E	540
1621	TCGTGGGTGAAACAAAGAAAAACAAGCTACACCCATATCATCTCAAGAACATGCAACT	1680
541	S W G G T K E K Q A Y T H I I F K N A T	560
1681	TTTACATTACATGGCATTCCAGAGAACTAATCAGGTCAAGATAATAGACGGTTCATC	1740
561	F T F T W A F Q R T N Q G Q D N R R F I	580
1741	AATGACATGGTGAAGATTATTCTATCACAGCCACTAATGCAGTTGATGGGTGGCGTCC	1800
581	N D M V K I Y S I T A T N A V D G V A S	600
1801	TCATGCCGTGCCTGTGCCCTCGTTCTGAACAGTCGGTTCATCGTGTCCCCCTGCCCT	1860
601	S C R A C A L G S E Q S - G S S C V P C P	620
1861	CCAGGCCACTACATTGAGAAAGAAACCAACCAACAGTGCAAGGAATGTCCACCTGACACCTAC	1920
621	P G H Y I E K E T N Q C K E C P P D T Y	640
1921	CTGTCACATCAGGTCTATGGAAAGAGGGCTGTATTCCATGGGGCTGGAGTAAA	1980
641	L S I H Q V Y G K E A C I P C G P G S K	660
1981	AACAATCAGGACCATTGGTTGGCTATAGTGAUTGCTTTCTACCATGAAAAAGAAAAT	2040
661	N N Q D H S V C Y S D C F F Y H E K E N	680
2041	CAGATTTGCACTATGACTTACCGAACCTCAGCAGTGTGGCTATTAATGAATGGCCCC	2100
681	Q I L H Y D F S N L S S V G S L M N G P	700
2101	AGCTTCACCTCCAAAGGAACAAAATACCTCCATTCTCAATATCAGTTATGTGGCAT	2160
701	S F T S K G T K Y F H F F N I S L C G H	720

2161	GAGGGGAAGAAGATGGCTCTGTACCAACAATATAACAGACTTACAGTAAAAGAAATA	2220
721	E G K K M A L C T N N I T D F T V K E I	740
2221	GTGGCAGGGTCAGATGATTACACAAATTGGTAGGGCATTGTATGCCAGTCACAATT	2280
741	V A G S D D Y T N L V G A F V C Q S T I	760
2281	ATTCCTCTGAAAGTAAGGGTTCCGAGCAGCCTTATCATCACAAATCCATCATTGGCA	2340
761	I P S E S K G F R A A L S S Q S I I L A	780
2341	GATACATTCAAGGAGTCACAGTTGAAACCACATTGAAAAATTAAATATAAAAGAAGAT	2400
781	D T F I G V T V E T T L K N I N I K E D	800
2401	ATGTTCCCAGTTCCAACAAGCAAATACCAAGATGTGCATTCTTATAAGTCTTCTACA	2460
801	M F P V P T S Q I P D V H F F Y K S S T	820
2461	GCAACAAACATCTGTATTAATGCCGATCAACTGCTGTGAAATGAGGTGAATCCTACT	2520
821	A T T S C I N G R S T A V K M R C N P T	840
2521	AAATCTGGAGCAGGAGTGATTCAGTCCCCAGCAAGTGCCAGCAGGTACCTGTGATGGG	2580
841	K S G A G V I S V P S K C P A G T C D G	860
2581	TGTACGTTCTATTCCTGTGGAGAGTGCTGAAGCTTGCCTCTGTGTACGGAGCATGAC	2640
861	C T F Y F L W E S A E A C P L C T E H D	880
2641	TTCCATGAGATTGAGGGAGCCTGCAAGAGAGGATTCAAGAACCTTGTATGTGTGAAAT	2700
881	F H E I E G A C K R G F Q E T L Y V W N	900
2701	GAACCTAAATGGTGCATTAAAGGAATTCTTGCCTGAGAAAAGTGGCACACCTGTGAA	2760
901	E P K W C I K G I S L P E K K L A T C E	920
2761	ACGGTTGACTTTGGCTGAAGGTGGAGCCGGTGTGGAGCTTTACTGCCGTTTGCTG	2820
921	T V D F W L K V G A G V G A F T A V L L	940
2821	GTGGCTCTGACCTGCTACTTCTGGAAAAAGAATCAAAACTGGAATACAAATATTCAAG	2880
941	V A L T C Y F W K K N Q K L E Y K Y S K	960

FIG. 4D

2881	TTAGTAATGACGACTAACTCAAAAGAGTGTGAACCTCCGGCTGCAGACAGTTGTGCTATC	2940
961	L V M T T N S K E C E L P A A D S C A I	980
2941	ATGGAAGGAGAAGATAATGAAGAGGAAGTTGTATATTCCAATAAACAGTCACTAGGA	3000
981	M E G E D N E E E V V Y S N K Q S L L G	1000
3001	AAACTCAAATCTTGGCAACCAAGGAAAAAGAAGACCATTGAAATCTGTTCACTGAAA	3060
1001	K L K S L A T K E K E D H F E S V Q L K	1020
3061	ACCTCAAGATCCCCAAATATATGAAGAGACAGTGCTGTAGCCTTGAGACTAATGAACAAA	3120
1021	T S R S P N I *	1028
3121	GAAACCTGCTCTAGTTTACAGGACCATTAGGTCTGCTCTACACGTACATT	3180
3181	GGTGATCTCACAGAGGAGGGCATGCCGCTGAAAGGGAAAGGAGATTGAAACATTGATT	3240
3241	GCCTTATCACATGGTCAAGTACCTGCCAAATAAGGAAAGCAAATGATTGGTCTCAA	3300
3301	CTGAAGATGAAGCTCAACTCAGGAAGAGATTATCTGTATATACACATAACTGAAAACCA	3360
3361	AGTTTAAGCCCACCAATGCACTGCTGATGCCATATAATTATGGTAACTTTATT	3420
3421	CTTTATGATGTCTACATAACAAGTGTGATTGGAAGGCACATGTGAGCATATGCCATTATG	3480
3481	ATCCAATTATGTTTTCTTGTATATTTGGGAAAATTAAAATTTTTAAGGTAA	3540
3541	AAAAAAAAAAAAAAA 3556	

FIG. 4E

S E R I E S 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20

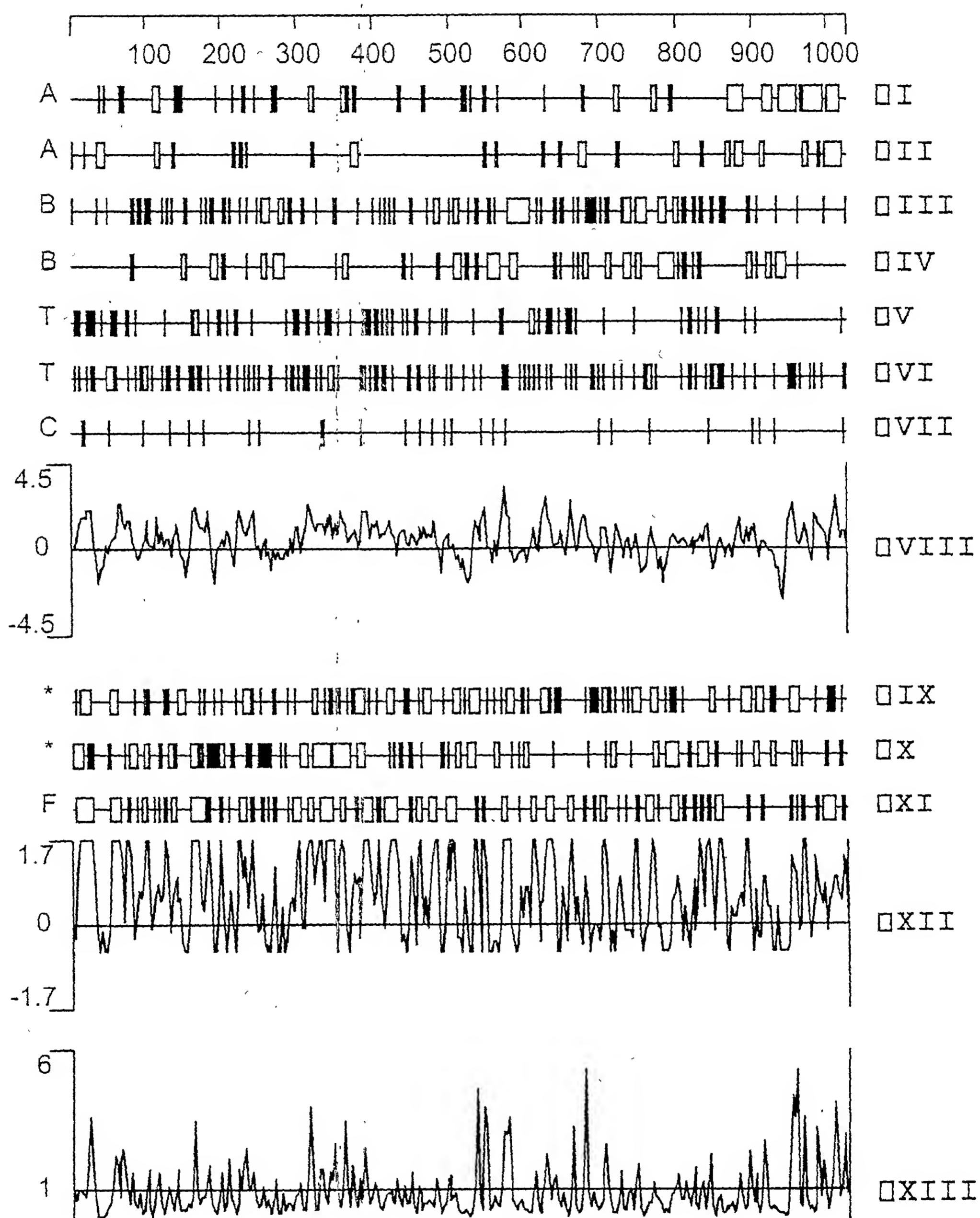


FIG. 5

	10	20	30	40	
1	MLFRARGPVRGRGWRPAEAPRRGRSPPWSPA WI C C W A L A				SEQ ID 2 SEC10
1	-----	-----	-----	-----	-----
	50	60	70	80	
41	GCQAAWAGDLPSSSRPLPPCQEKDYHFEYTECDSSGSRW				SEQ ID 2 SEC10
1	-----	-----	-----	-----	-----
	90	100	110	120	
81	RVAIPNSAVDCSGLPD P V R G K E C T F S C A S G E Y L E M K N Q V C				SEQ ID 2 SEC10
1	-----	-----	-----	-----	-----
	130	140	150	160	
121	SKCGEGTYSLGSGIKFDEWDEL PAGEFSNIATFMDTVVGPS				SEQ ID 2 SEC10
7	SKCGEGTYSLGSGIKFDEWDEL PAGEFSNIATFMDTVVGPS				
	170	180	190	200	
161	DSRPDGCGNNSSWI PRGNYIESNRDDCTVSLIYAVHLKKSG				SEQ ID 2 SEC10
47	DSRPDGCGNNSSWI PRGNYIESNRDDCTVSLIYAVHLKKSG				
	210	220	230	240	
201	YVFFEYQYVDNNIFFEFIQNDQCQEMDTT D KWVKLTDN				SEQ ID 2 SEC10
87	YVFFEYQYVDNNIFFEFIQNDQCQEMDTT D KWVKLTDN				
	250	260	270	280	
241	GEWGSHSVMLKSGTNILYWR TTGILMGSKAVKPVLVKNIT				SEQ ID 2 SEC10
127	GEWGSHSVMLKSGTNILYWR TTGILMGSKAVKPVLVKNIT				
	290	300	310	320	
281	I E G V A Y T S E C F P C K P G T F S N K P G S F N C Q V C P R N T Y S E K G A				SEQ ID 2 SEC10
167	I E G V A Y T S E C F P C K P G T F S N K P G S F N C Q V C P R N T Y S E K G A				
	330	340	350	360	
321	K E C I R C K D D S Q F S - G S S E C T E R P P C T T K D Y F Q I H T P C D E				SEQ ID 2 SEC10
207	K E C I R C K D D S Q F S E E G S S E C T E R P P C T T K D Y F Q I H T P C D E				
	370	380	390	400	
359	E G K T Q I M Y K W I E P K I C R E D L T D A I R L P P S G E K K D C P P C N P				SEQ ID 2 SEC10
247	E G K T Q I M Y K W I E P K I C R E D L T D A I R L P P S G E K K D C P P C N P				
	410	420	430	440	
399	G F Y N N G S S S C H P C P P G T F S D G T K E C R P C P A G T E P A L G F E Y				SEQ ID 2 SEC10
287	G F Y N N G S S S C H P C P P G T F S D G T K E C R P C P A G T E P A L G F E Y				
	450	460	470	480	
439	K W W N V L P G N M K T S C F N V G N S K C D G M N G W E V A G D H I Q S G A G				SEQ ID 2 SEC10
327	K W W N V L P G N M K T S C F N V G N S K C D G M N G W E V A G D H I Q S G A G				
	490	500	510	520	
479	G S D N D Y L I L N L H I P G F K P P T S M T G A T G S E L G R I T F V F E T L				SEQ ID 2 SEC10
367	G S D N D Y L I L N L H I P G F K P P T S M T G A T G S E L G R I T F V F E T L				

FIG. 6A

	530	540	550	560	
519	CSADCVL YFMVDINRKSTNVVESWGKTKEKQAYTHIIFKN				SEQ ID 2
407	CSADCVL YFMVDINRKSTNVVESWGKTKEKQAYTHIIFKN				SEC10
	570	580	590	600	
559	ATFTFTWAFQR TNQGQDNRRFINDMVKIYSITATNAVDGV				SEQ ID 2
447	ATFTFTWGIPIRE - - - - -				SEC10
	610	620	630	640	
599	ASSCRACALGSEQSGSSCVPCPPGHYIEKE TNQCKECPD				SEQ ID 2
459	- - - - -				SEC10
	650	660	670	680	
639	TYLSIHQVYKGAEACIPCGPGSKNNQDH SVCYSDCFYHEK				SEQ ID 2
459	- - - - -				SEC10
	690	700	710	720	
679	ENQILHYDFSNLSSVGSLMN GPR SFTSKGTKYFHFFNISLC				SEQ ID 2
459	- - - - - LIQGPR				SEC10
	730	740	750	760	
719	GHEGKKMALCTNNITDFTVKEIVAGSDDYTNLVGAFVCQS				SEQ ID 2
464	- - - - -				SEC10
	770	780	790	800	
759	TIIIPSeskGFRAALSSQSIILADTFIGVTVE TTLKNINIK				SEQ ID 2
464	- - - - -				SEC10
	810	820	830	840	
799	EDMFPVPTSQIPDVHFFYKSSTATSCINGRSTA VKMRCN				SEQ ID 2
464	- - - - -				SEC10
	850	860	870	880	
839	PTKSGAGVISVPSKCPAGTC DGCTFYFLWE SA EACPLCTE				SEQ ID 2
464	- - - - -				SEC10
	890	900	910	920	
879	HDFHEIEGACKRGFQETLYVWN EPKWCIGISLPEKKLAT				SEQ ID 2
464	- - - - -				SEC10
	930	940	950	960	
919	CETVDFWLKVGA GVGAFTAVLLVALTCYFWKKNQKKKKTI				SEQ ID 2
464	- - - - -				SEC10
	LNLFN				SEQ ID 2
959	- - - - -				SEC10

Decoration 'Decoration #1': Shade (with solid black) residues that match the consensus named 'Consensus #1' exactly.

FIG. 6B

	10	20	30	40	
1	MLF RARGP V R G R G W G R P A E A P R R G R S P P W S P A W I C C W A L A				SEQ ID 4 SEC10
1	-----				-----
	50	60	70	80	
41	G C Q A A W A G D L P S S S R P L P P C Q E K D Y H F E Y T E C D S S G S R W				SEQ ID 4 SEC10
1	-----				-----
	90	100	110	120	
81	R V A I P N S A V D C S G L P D P V R G K E C T F S C A S G E Y L E M K N Q V C				SEQ ID 4 SEC10
1	-----				-----
	130	140	150	160	
121	S K C G E G T Y S L G S G I K F D E W D E L P A G E F S N I A T F M D T V V G P S				SEQ ID 4 SEC10
7	S K C G E G T Y S L G S G I K F D E W D E L P A G E F S N I A T F M D T V V G P S				SEC10
	170	180	190	200	
161	D S R P D G C N N S S W I P R G N Y I E S N R D D C T V S L I Y A V H L K K S G				SEQ ID 4 SEC10
47	D S R P D G C N N S S W I P R G N Y I E S N R D D C T V S L I Y A V H L K K S G				SEC10
	210	220	230	240	
201	Y V F F E Y Q Y V D N N I F F E F F I Q N D Q C Q E M D T T T D K W V K L T D N				SEQ ID 4 SEC10
87	Y V F F E Y Q Y V D N N I F F E F F I Q N D Q C Q E M D T T T D K W V K L T D N				SEC10
	250	260	270	280	
241	G E W G S H S V M L K S G T N I L Y W R T T G I L M G S K A V K P V L V K N I T				SEQ ID 4 SEC10
127	G E W G S H S V M L K S G T N I L Y W R T T G I L M G S K A V K P V L V K N I T				SEC10
	290	300	310	320	
281	I E G V A Y T S E C F P C K P G T F S N K P G S F N C Q V C P R N T Y S E K G A				SEQ ID 4 SEC10
167	I E G V A Y T S E C F P C K P G T F S N K P G S F N C Q V C P R N T Y S E K G A				SEC10
	330	340	350	360	
321	K E C I R C K D D S Q F S - G S S E C T E R R P P C T T K D Y F Q I H T P C D E				SEQ ID 4 SEC10
207	K E C I R C K D D S Q F S E E G S S E C T E R R P P C T T K D Y F Q I H T P C D E				SEC10
	370	380	390	400	
359	E G K T Q I M Y K W I E P K I C R E D L T D A I R L P P S G E K K D C P P C N P				SEQ ID 4 SEC10
247	E G K T Q I M Y K W I E P K I C R E D L T D A I R L P P S G E K K D C P P C N P				SEC10
	410	420	430	440	
399	G F Y N N G S S S C H P C P P G T F S D G T K E C R P C P A G T E P A L G F E Y				SEQ ID 4 SEC10
287	G F Y N N G S S S C H P C P P G T F S D G T K E C R P C P A G T E P A L G F E Y				SEC10
	450	460	470	480	
439	K W W N V L P G N M K T S C F N V G N S K C D G M N G W E V A G D H I Q S G A G				SEQ ID 4 SEC10
327	K W W N V L P G N M K T S C F N V G N S K C D G M N G W E V A G D H I Q S G A G				SEC10
	490	500	510	520	
479	G S D N D Y L I L N L H I P G F K P P T S M T G A T G S E L G R I T F V F E T L				SEQ ID 4 SEC10
367	G S D N D Y L I L N L H I P G F K P P T S M T G A T G S E L G R I T F V F E T L				SEC10

FIG. 7A

	530	540	550	560	
519	C S A D C V L Y F M V D I N R K S T N V V E S W G G T K E K Q A Y T H I I F K N				SEQ ID 4
407	C S A D C V L Y F M V D I N R K S T N V V E S W G G T K E K Q A Y T H I I F K N				SEC10
	570	580	590	600	
559	A T F T F T W A F Q R T N Q G Q D N R R F I N D M V K I Y S I T A T N A V D G V				SEQ ID 4
447	A T F T F T W G I P R E - - - - -				SEC10
	610	620	630	640	
599	A S S C R A C A L G S E Q S G S S C V P C P P G H Y I E K E T N O C K E C P P D				SEQ ID 4
459	- - - - -				SEC10
	650	660	670	680	
639	T Y L S I H Q V Y G K E A C I P C G P G S K N N Q D H S V C Y S D C F F Y H E K				SEQ ID 4
459	- - - - -				SEC10
	690	700	710	720	
679	E N Q I L H Y D F S N L S S V G S L M N G P S F T S K G T K Y F H F F N I S L C				SEQ ID 4
459	- - - - - L I Q G P - - - - -				SEC10
	730	740	750	760	
719	G H E G K K M A L C T N N I T D F T V K E I V A G S D D Y T N L V G A F V C Q S				SEQ ID 4
464	- - - - -				SEC10
	770	780	790	800	
759	T I I P S E S K G F R A A L S S Q S I I L A D T F I G V T V E T T L K N I N I K				SEQ ID 4
464	- - - - -				SEC10
	810	820	830	840	
799	E D M F P V P T S Q I P D V H F F Y K S S T A T T S C I N G R S T A V K M R C N				SEQ ID 4
464	- - - - -				SEC10
	850	860	870	880	
839	P T K S G A G V I S V P S K C P A G T C D G C T F Y F L W E S A E A C P L C T E				SEQ ID 4
464	- - - - -				SEC10
	890	900	910	920	
879	H D F H E I E G A C K R G F Q E T L Y V W N E P K W C I K G I S L P E K K L A T				SEQ ID 4
464	- - - - -				SEC10
	930	940	950	960	
919	C E T V D F W L K V G A G V G A F T A V L L V A L T C Y F W K K N Q K L E Y K Y				SEQ ID 4
464	- - - - -				SEC10
	970	980	990	1000	
959	S K L V M T T N S K E C E L P A A D S C A I M E G E D N E E E V V Y S N K Q S L				SEQ ID 4
464	- - - - -				SEC10
	1010	1020	1030		
999	L G K L K S L A T K E K E D H F E S V Q L K T S R S P N I .				SEQ ID 4
464	- - - - - R				SEC10

Decoration 'Decoration #1': Shade (with solid black) residues that match the consensus named 'Consensus #1' exactly.

FIG. 7B